IN THE CLAIMS

Please substitute the following claim set for those currently of record:

1. -34. (Cancelled)

35. (Original) A method for analyzing nucleotide sequence variations, comprising:

forming microemulsions comprising one or more species of analyte DNA molecules;

amplifying analyte DNA molecules in the microemulsions in the presence of reagent beads, wherein the reagent beads are bound to a plurality of molecules of a primer for amplifying the analyte DNA molecules, whereby product beads are formed which are bound to a plurality of copies of one species of analyte DNA molecule;

separating the product beads from analyte DNA molecules which are not bound to product beads;

determining a sequence feature of the one species of analyte DNA molecule which is bound to the product beads.

36. (Original) The method of claim 35 further comprising the step of isolating product beads which are bound to a plurality of copies of a first species of analyte DNA molecule from product beads which are bound to a plurality of copies of a second species of analyte DNA molecule.

37. (Original) The method of claim 36 wherein the step of isolating is performed using fluorescence activated cell sorting.

38. (Original) The method of claim 36 further comprising the step of recovering the first species of analyte DNA molecule from the product beads.

39. (Original) The method of claim 36 further comprising the step of amplifying the first species of analyte DNA molecule from the isolated product beads.

40. (Original) The method of claim 38 further comprising the step of determining the sequence of the first species of analyte DNA molecule.

41. (Original) The method of claim 35 wherein the step of amplifying converts less than 10 % of the reagent beads present in the microemulsions into product beads.

42. (Original) The method of claim 35 wherein prior to the step of separating, the microemulsions are broken by addition of one or more detergents.

43. (Original) The method of claim 35 wherein the step of determining is performed by hybridization to oligonucleotide probes which are differentially labeled.

44. (Original) The method of claim 35 wherein the relative or absolute amounts of product beads comprising one or more sequence features is determined.

45. (Original) The method of claim 44 wherein the relative or absolute amounts are determined using flow cytometry.

46. (Original) The method of claim 35 wherein the step of amplifying employs additional copies of the primer which are not bound to the reagent bead.

47. (Original) The method of claim 35 wherein the analyte DNA molecules are genomic DNA.

48. (Original) The method of claim 35 wherein the analyte DNA molecules are cDNA.

49. (Original) The method of claim 35 wherein the analyte DNA molecules are PCR products made from genomic DNA.

50. (Original) The method of claim 35 wherein the analyte DNA molecules are PCR products made from cDNA.

51. (Original) The method of claim 35 wherein the analyte DNA molecules are derived from a single individual.

52. (Original) The method of claim 35 wherein the analyte DNA molecules are derived from a population of individuals.

53. (Original) The method of claim 35 wherein the reagent beads are magnetic.

54. (Original) The method of claim 35 wherein the step of determining a sequence feature is performed by extension of a primer with one or more labeled deoxyribonucleotides.

55. -58. (Cancelled)

59. (Original) A method for isolating nucleotide sequence variants, comprising:

forming microemulsions comprising one or more species of analyte DNA molecules;

amplifying analyte DNA molecules in the microemulsions in the presence of reagent beads, wherein the reagent beads are bound to a plurality of molecules of a

primer for amplifying the analyte DNA molecules, whereby product beads are formed which are bound to a plurality of copies of one species of analyte DNA molecule;

separating the product beads from analyte DNA molecules which are not bound to product beads;

isolating product beads which are bound to a plurality of copies of a first species of analyte DNA molecule from product beads which are bound to a plurality of copies of a second species of analyte DNA molecule.

60. (Original) The method of claim 59 wherein the step of isolating is performed using fluorescence activated cell sorting.

61. (Original) The method of claim 59 further comprising the step of recovering the first species of analyte DNA molecule from the product beads.

62. (Original) The method of claim 59 further comprising the step of amplifying the first species of analyte DNA molecule from the isolated product beads.

63. (Original) The method of claim 59 further comprising the step of determining the sequence of the first species of analyte DNA molecule.

64. -84.(Cancelled)